

Fig. 1

(A) FBD(1,2) fused at the C-terminal of SK

| | | |
|----|---|---|
| SK | 1 | 2 |
|----|---|---|

(B) FBD(4,5) fused at the C-terminal of SK

| | | |
|----|---|---|
| SK | 4 | 5 |
|----|---|---|

(C) FBD(4,5) fused at the N-terminal of SK

| | | |
|---|---|----|
| 4 | 5 | SK |
|---|---|----|

(D) FBD(4,5) fused at both the C as well as N-terminals of SK

| | | | | |
|---|---|----|---|---|
| 4 | 5 | SK | 4 | 5 |
|---|---|----|---|---|

Fig. 2

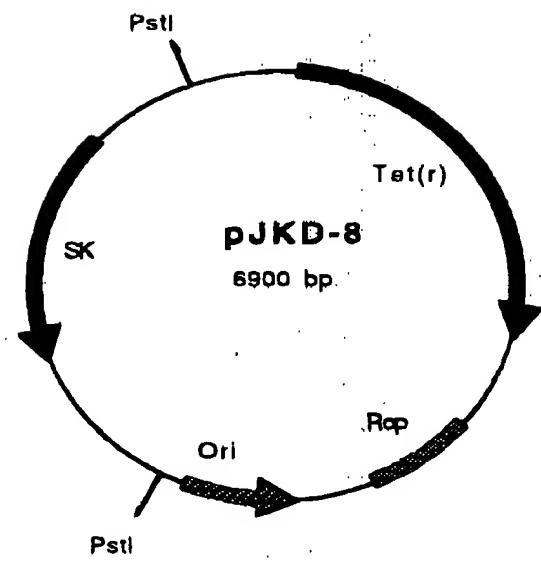


Fig. 3

1/1 31/11
 ATT GCT GGA CCT GAG TGG CTG CTA GAC CGT CCA TCT GTC AAC AAC AGC CAA TTA GTT GTC
 ile ala gly pro glu thr leu leu asp arg pro ser val asn asn ser gln leu val val
 61/21 91/31
 AGC GTT GCT GGT ACT GTT GAC GGG ACG AAT CAA GAC ATT AGT CTT AAA TTT TTT GAA ATC
 ser val ala gly thr val glu gly thr asn gln asp ile ser leu lys phe phe glu ile
 121/41 151/51
 GAT CTA ACA TCA CGA CCT GCT CAT GGA CGA AAG ACA GAG CAA GGC TTA AGT CCA AAA TCA
 asp leu thr ser arg pro ala his gly gly lys thr glu gln gly leu ser pro lys ser
 181/61 211/71
 AAA CCA TTT CCT ACT GAT AGT GGC GCG ATC TCA CAT AAA CTT GAG AAA GCT GAC TTA CTA
 lys pro phe ala thr asp ser gly ala met ser his lys leu glu lys ala asp leu leu
 241/81 271/91
 AAG GCT ATT CAA GAA CAA TTG ATC GCT AAC GTC CAC ACT AAC GAC GAC TAC TTT GAG GTC
 lys ala ile gln glu gln leu ile ala asn val his ser asp asp tyr phe glu val
 301/101 331/111
 ATT GAT TTT GCA AGC GAT GCA ACC ATT ACT GAT CGA AAC GGC AAG GTC TAC TTT GCT GAC
 ile asp phe ala ser asp ala thr ile thr asp arg ash gly lys val tyr phe ala asp
 361/121 391/131
 AAA GAT CGT TTG GTC ACC TTG CCG ACC CAA CCT GTC CAA GAA TTT TTG CTA AGC CGA CAT
 lys asp gly ser val thr leu pro thr gln pro val gln glu phe leu leu ser gly his
 421/141 451/151
 GIG CGC GTT AGA CCA TAT AAA GAA AAA CCA ATA CAA AAC CAA GCG AAA TCT GTT GAT GTG
 val arg val arg pro tyr lys glu lys pro ile gln asn gln ala lys ser val asp val
 481/161 511/171
 GAA TAT ACT GTC CAG TTT ACT CCC TTA AAC CCT GAT GAC GAT TTC AGA CCA CGT CTC AAA
 glu tyr thr val gln phe thr pro leu asn pro asp asp asp phe arg pro gly leu lys
 541/181 571/191
 GAT ACT AAG CTA TTG AAA ACA CTA GCT ATC GGT GAC ACC ATC ACA TCT CAA GAA TTA CTA
 asp thr lys leu leu lys thr leu ala ile gly asp thr ile thr ser gln glu leu leu
 601/201 631/211
 CCT CAA GCA CAA AGC ATT TTA AAC AAA AAC CAC CCA GGC TAT AGC ATT TAT GAA CGT GAC
 ala gln ala gln ser ile leu asn lys asn his pro gly tyr thr ile tyr glu arg asp
 661/221 691/231
 TCC TCA ATC GTC ACT CAT GAC AAT GAC ATT TTC CGT ACG ATT TTA CCA ATC GAT CAA GAG
 ser ser ile val thr his asp asn asp ile phe arg thr ile leu pro met asp gln glu
 721/241 751/251
 TTT ACT TAC CGT GTT AAA AAT CCG GAA CAA GCT TAT AGG ATC AAT AAA AAA TCT GGT CTG
 phe thr tyr arg val lys asn arg glu gln ala tyr arg ile asn lys ser gly leu
 781/261 811/271
 ATT CAA GAA ATA AAC AAC ACT GAC CTG ATC TCT GAG AAA TAT TAC GTC CTT AAA AAA CGG
 ash giv glu ile asn asn thr asp leu ile ser glu lys tyr tyr val leu lys gly
 841/281 871/291
 GAA AAG CCG TAT GAT CCC TTG GAT CGC AGT CAC TTG AAA CTG TTC ACC ATC AAA TAC GTT
 glu lys pro tyr asp pro phe asp arg ser his leu lys leu phe thr ile lys tyr val
 901/301 931/311
 GAT GTC GAT ACC AAC GAA TTG CTA AAA AGT GAG CAG CTC TTA ACA GCT AGC GAA CGT AAC
 asp val asp thr asn glu leu leu lys ser glu gln leu leu thr ala ser glu arg asn
 961/321 991/331
 TTA GAC TTG AGA GAT TTA TAC GAT CCT CGT GAT AAG GCT AAA CTA CTC TAC AAC AAT CTC
 leu asp phe arg asp leu tyr asp pro arg asp lys ala lys leu leu tyr asn asn leu
 1021/341 1051/351
 GAT GCT TTG GGT ATT ATG GAC TAT ACC TTA ACT GGA AAA GTC GAG GAT AAT CAC GAT GAC
 asp ala phe gly ile met asp tyr thr leu thr gly lys val glu asp asn his asp asp
 1081/361 1111/371
 ACC AAC CGT ATC ATA ACC TTG TAT ATG GGC AAG CGA CCC GAA GGA GAG AAT GCT AGC TAT
 thr asn arg ile ile thr val tyr met gly lys arg pro glu gly glu asn ala ser tyr
 1141/381 1171/391
 CAT TTA GCC TAT GAT AAA GAT CGT TAT ACC GAA GAA GAA GAA GAA GTT TAC ACC TAC CTC
 his leu ala tyr asp lys asp arg tyr thr glu glu glu arg glu val tyr ser tyr leu
 1201/401 1231/411
 CGT TAT ACA GGG ACA CCT ATA CCT GAT AAC CCT AAC GAC AAA TAA
 arg tyk thr gly thr pro ile pro asp asn pro asp lys OCH

Fig. 4

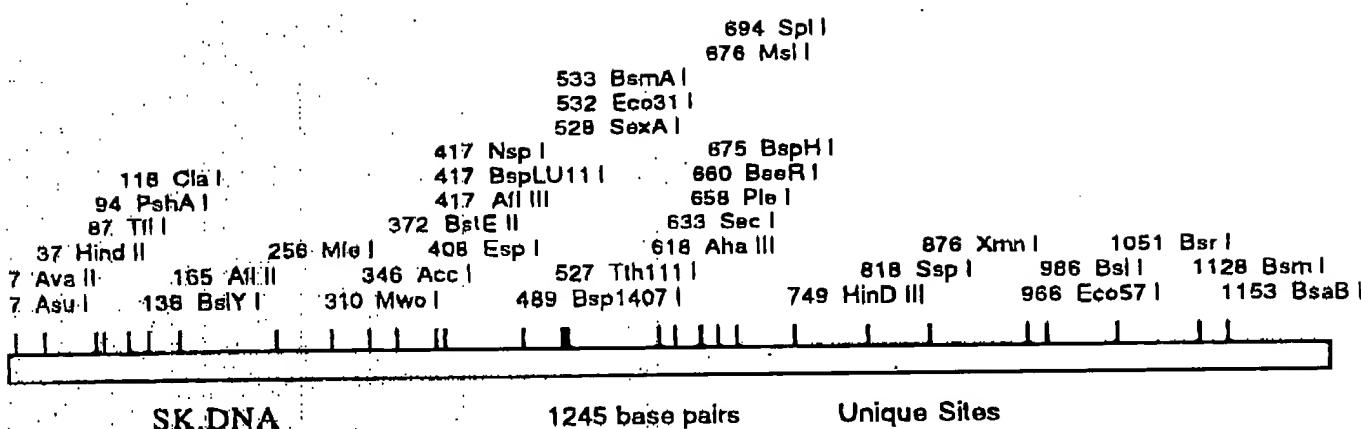


Fig. 5

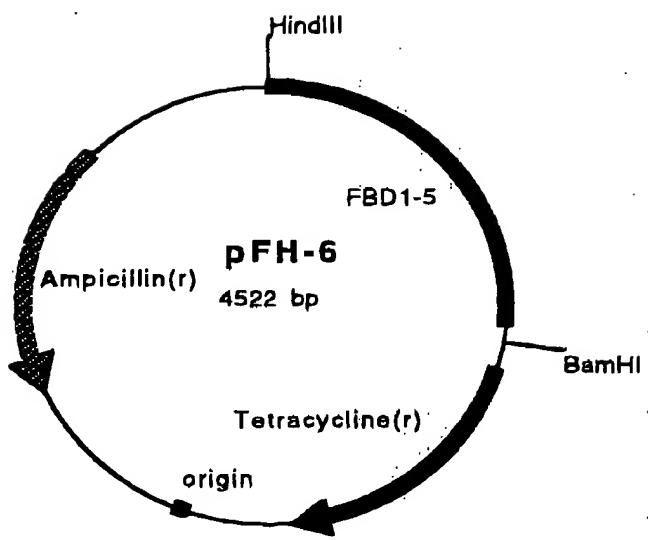


Fig. 6

31/11
1/1 CAG GCT CAG CAA ATG GTT CAG CCC CAG TCC CGG GTG CCT GTC ACT CAA AGC AAG CCC GGT
gln ala gln gln met val gln pro gln ser pro val ala val ser gln ser lys pro gly
61/21 91/31
TGT TAT GAC AAT GGA AAA CAC TAT CAG ATA AAT CAA CAG TGG GAG CGG ACC TAC CTA GGT
cys tyr asp asn gly lys his tyr gln ile asn gln gln trp glu arg thr tyr leu gly
121/41 151/51
AAT GTC TTG GTT TGT ACT TGT TAT GGA GGA AGC CGA CCT TTT AAC TGC GAA AGT AAA CCT
asn val leu val cys thr cys tyr gly gly ser arg gly phe asn cys glu ser lys pro
181/61 211/71
GAA GCT GAA GAG ACT TGC TTT GAC AAG TAC ACT GGG AAC ACT TAC CGA GTG GGT GAC ACT
glu ala glu glu thr cys phe asp lys tyr thr gly asn thr tyr arg val gly asp thr
241/81 271/91
TAT GAG CGT CCT AAA GAC TCC ATG ATC TGG GAC TGT ACC TGC ATC CGG CCT CGG CGA CCC
tyr glu arg pro lys asp ser met ile trp asp cys thr cys ile gly ala gly arg gly
301/101 331/111
AGA ATA ACC TGT ACC ATC GCA AAC CGC TGC CAT GAA CGG GGT CAG TCC TAC AAG ATT CCT
arg ile ser cys thr ile ala asn arg cys his glu gly gly gln ser tyr lys ile gly
361/121 391/131
GAC ACC TGG ACC AGA CCA CAT GAG ACT GGT GGT TAC ATG TTA GAG TGT GTG TGT CTT GGT
asp thr trp arg arg pro his glu thr gly gly tyr met leu glu cys val cys leu gly
421/141 451/151
AAT GGA AAA CGA GAA TGG ACC TGC AAG CCC ATA GCT GAG AAG TGT TTT GAT CAT GCT GCT
asn gly gln trp thr cys lys pro ile ala glu lys cys phe asp his ala ala
481/161 511/171
GGG ACT TCC TAT GTG GTC CGA GAA ACG TGG GAG AAG CCC TAC CAA CGC TGG ATG ATG GTA
gly thr ser tyr val val gly glu thr trp glu lys pro tyr gln gly trp met met val
541/181 571/191
GAT TGT ACT TGC CTG CGA GAA CGC AGC CGA CGC ATC ACT TGC ACT TCT AGA AAT AGA TCC
asp cys thr cys leu gly glu gly ser gly arg ile thr cys thr ser arg asn arg cys
601/201 631/211
AAC GAT CAG GAC ACA ACG ACA TCC TAT AGA ATT GGA GAC ACC TGG ACC AAC AAG GAT AAT
asn asp gln asp thr arg thr ser tyr arg ile gly asp thr trp ser lys lys asp asn
661/221 691/231
CGA GGA AAC CTG CTC CAG TGC ATC TGC ACA CGC AAC CGC CGA CGA GAG TGG AAG TGT GAG
arg gly asn leu leu gln cys ile cys thr gly asn gly arg gly glu trp lys cys glu
721/241 751/251
AGG CAC ACC TCT GTG CAG ACC ACA TCG AGC GGA TCT CGC CCC TTC ACC GAT GTT CGT
arg his thr ser val gln thr ser ser gly ser gly pro phe thr asp val arg

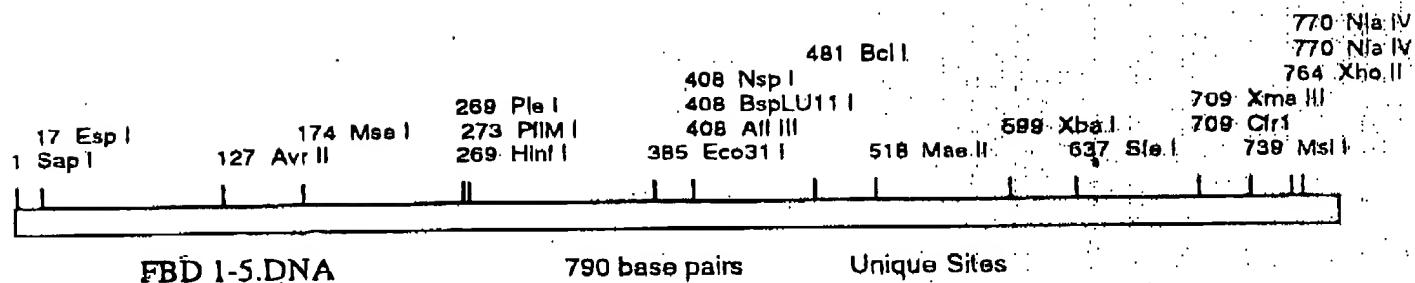
Fig. 7

Fig. 8

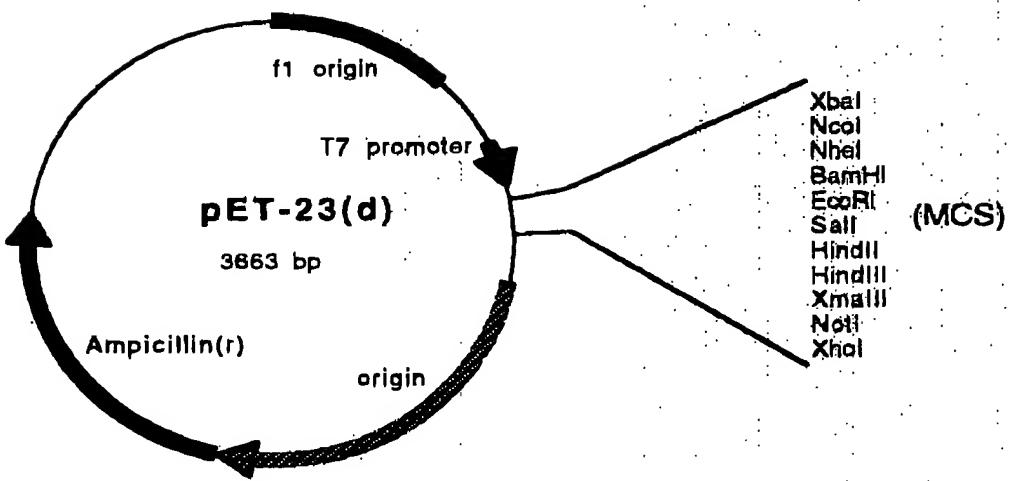


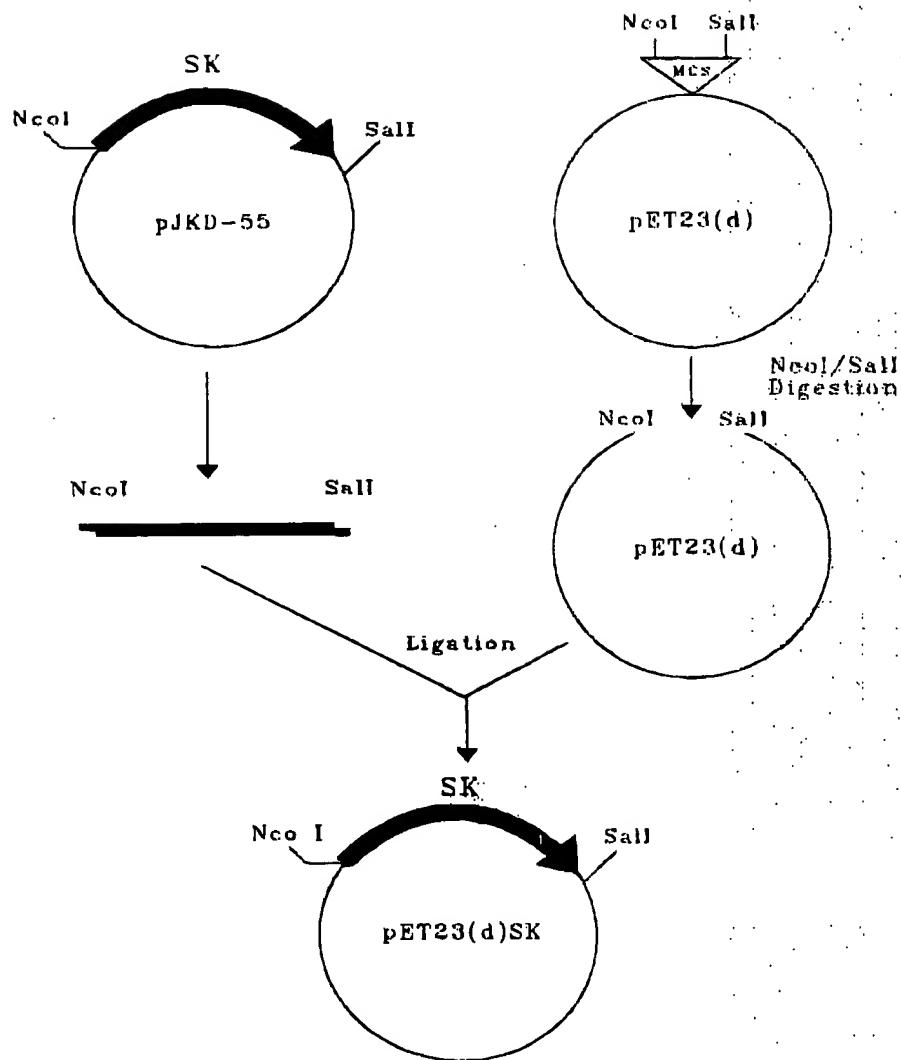
Fig. 9

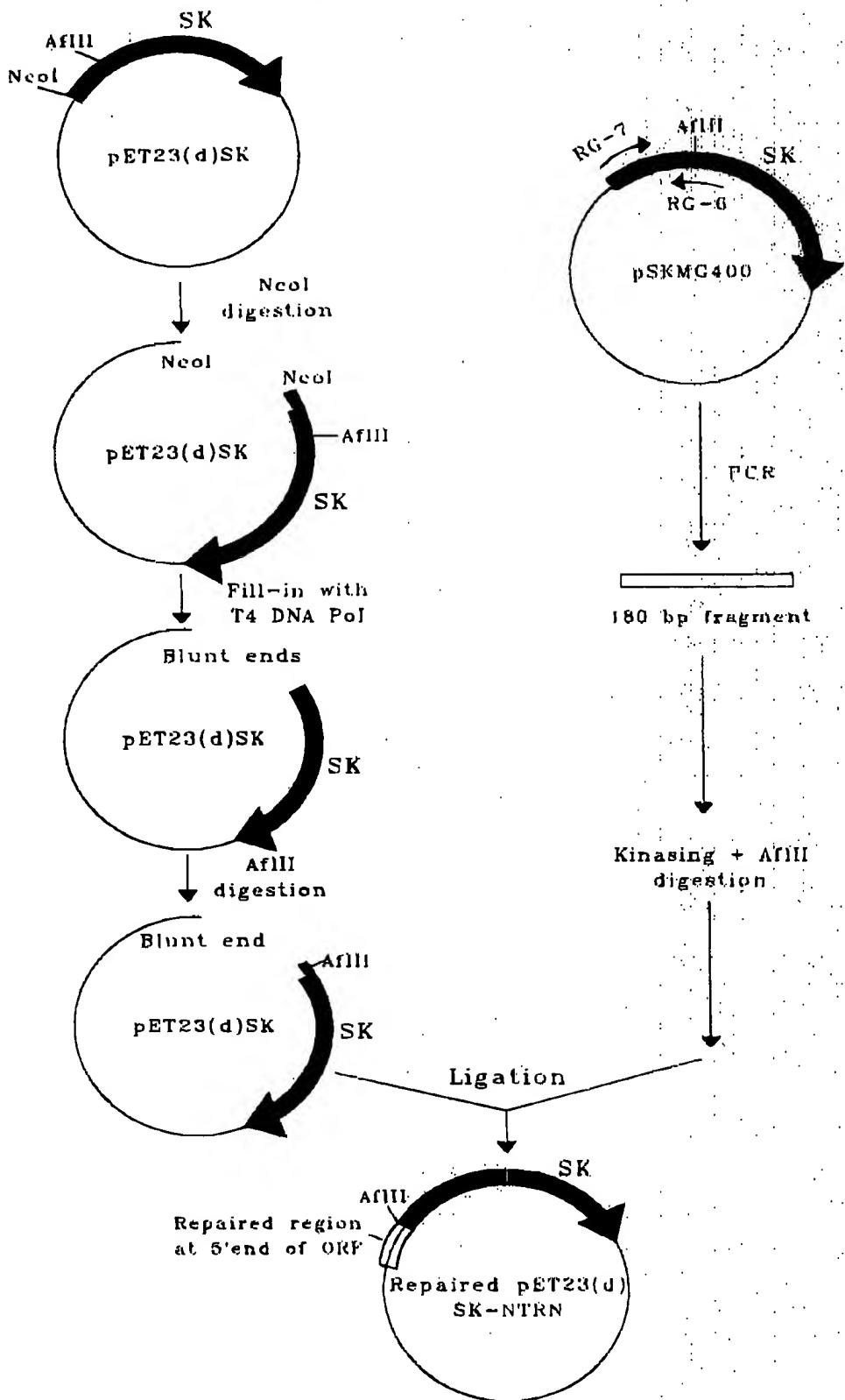
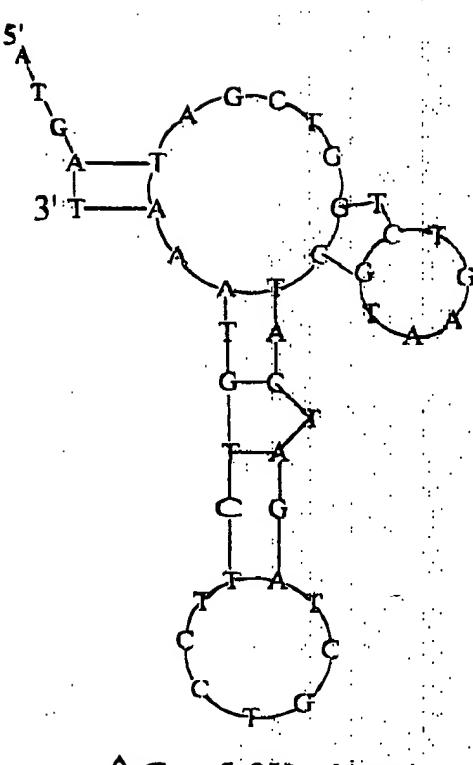
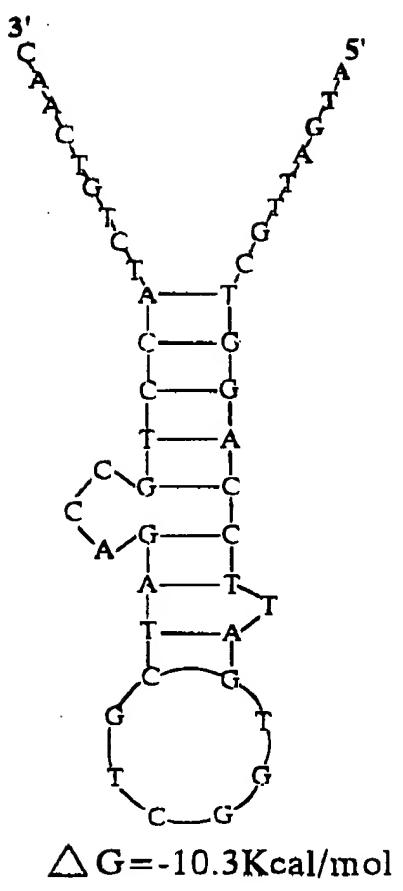
Fig. 10

Fig. 11

| | 10 | 20 | 30 | 40 | 50 |
|------|-------------|-------------|-------------|-------------|-------------|
| 51 | GCACCCGTGG | CCAGGACCCA | ACGCTGCCG | AGATCTCGAT | CCCCCGAAAT |
| 101 | TAATACGAET | CACTATAGGG | AGACCACAAC | GGTTTCCCTC | TAGAAAATAAT |
| 151 | TTTGTAAAC | TTAAGAAGG | AGATATAACCA | TGATTGCTGG | ACCTGAGTGG |
| 201 | CTGCTAGACC | GTCCATCTGT | CAACAAACAGC | CAATTGGTTG | TTAGCGTTGC |
| 251 | TGGTACTGTT | GAGGGGACGA | ATCAAGACAT | TAGTCTTAAA | TTTTTTGAAA |
| 301 | TCGATCTAAC | ATCACGACCT | GCTCATGGAG | GAAAGACAGA | GCAAGGCTTA |
| 351 | AGTCCAAAAT | CAAACCATT | TGCTACTGAT | AGTGGCGCGA | TGTCACATAA |
| 401 | ACTTGAGAAA | GCTGACTTAC | TAAAGGCTAT | TCAAGAACAA | TTGA1CCCTA |
| 451 | ACGTCCACAG | TAACGACGAC | TACTTTGAGG | TCATTGATT | TGCAAGEGAT |
| 501 | GCAACCATT | CTGATCGAAA | CGGCAAGGTC | TACTTTGCTG | ACAAACATGG |
| 551 | TTCGGTAACC | TTGCCGACCC | AACCTGTCCA | AGAATTTTG | CTAACCGGAC |
| 601 | ATGTGCGCGT | TAGACCATAT | AAAGAAAAAC | CAATACAAAA | CCAAGCGAAA |
| 651 | TCTGTTGATG | TGGAATATAC | TGTACAGTTT | ACTCCCTTAA | ACCCCTGATGA |
| 701 | CGATTCAGA | CCAGGTCTCA | AAGATACTAA | GCTATTGAAA | ACACTAGCTA |
| 751 | TCGGTGACAC | CATCACATCT | CAAGAATTAC | TAGCTCAAGC | ACAAAGCATT |
| 801 | TTAAACAAAAA | ACCACCCAGG | CTATACGATT | TATGAACGTG | ACTCCTCAAT |
| 851 | CGTCACTCAT | GACAATGACA | TTTCCGTAC | GATTITACCA | ATGGATCAAG |
| 901 | AGTTTACTTA | CCGTGTTAAA | AATCGGGAAC | AAGCTTATAG | GATCAATAAA |
| 951 | AAATCTGGTC | TGAATGAAGA | AATAAACAAAC | ACTGACCTGA | TCTCTGAGAA |
| 1001 | ATATTACGTC | CTTAAAAAAAG | GGGAAAAGCC | GTATGATCCC | TTTGATCGCA |
| 1051 | GTCACTTGAA | ACTGTTCAAC | ATCAAATACG | TTGATGTCGA | TACCAACGAA |
| 1101 | TTGCTAAAAAA | GTGAGCAGCT | CTTAAACAGCT | AGCGAACGTA | ACITAGACTT |
| 1151 | CAGAGATITA | TACGATCCTC | GTGATAAGGC | TAAACTACTC | TACAACAATC |
| 1201 | TCGATGCTTT | TGGTATTATG | GAECTATACCT | TAACCTGGAAA | AGTAGAGGAT |
| 1251 | AATCACGATG | ACACCAACCG | TATCATAACC | GTITATATGG | GCAAGGGACC |
| 1301 | CGAAGGAGAG | AATGCTAGCT | ATCATTAGC | CTATGATAAA | GATCGTTATA |
| 1351 | CCGAAGAAGA | ACGAGAAGTT | TACAGCTACC | TGCGTTATAC | AGGGACACCT |
| | ATACCTGATA | ACCCCTAACGA | CAAATAA | | |

Fig. 12



$$\Delta G = -10.3 \text{ Kcal/mol}$$

(A)

$$\Delta G = -5.0 \text{ Kcal/mol}$$

(B)

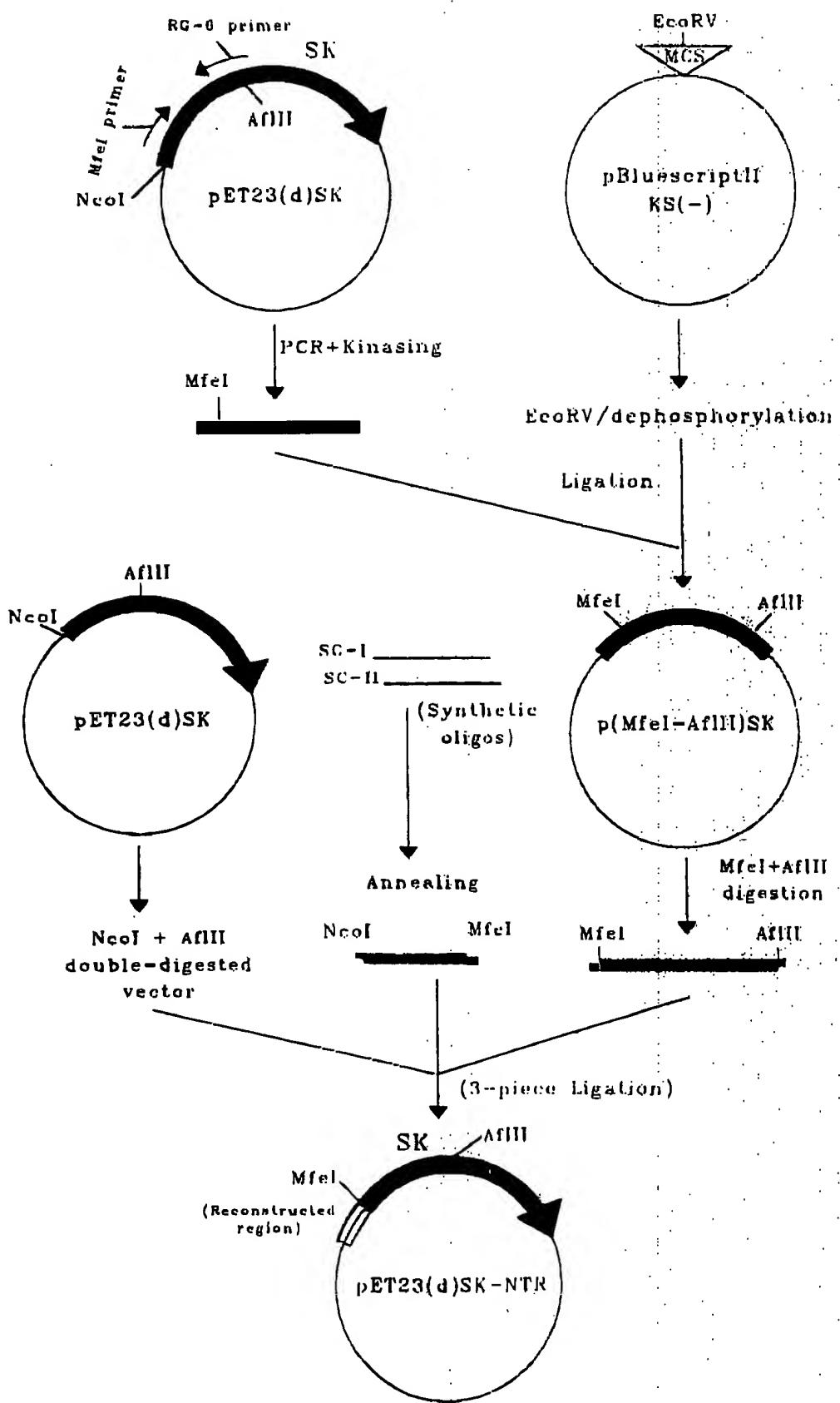
Fig. 13

Fig. 14

| | 10 | 20 | 30 | 40 | 50 |
|------|-------------|------------|-------------|-------------|-------------|
| 51 | TAATACGACT | CACTATAGGG | AGACCACAAC | GGTTCCCTC | TAGAAATAAT |
| 101 | TTTGTAAAC | TTAAGAAGG | AGATATAACCA | TGATAGCTGG | TCCGTGAATGG |
| 151 | CTACTAGATC | GTCCTTCTGT | AAATAACAGC | CAATTGGTTG | TTAGCGTTIGC |
| 201 | TGGTACTGTT | GAGGGGACGA | ATCAAGACAT | TAGTCTAAA | TTTTTTGAAA |
| 251 | TCGATCTAAC | ATCACGACCT | GCTCATGGAG | GAAAGACAGA | GCAAGGCTTA |
| 301 | AGTCCAAAAT | CAAACCAATT | TGCTACTGAT | AGTGGCGCGA | TGTCACATAA |
| 351 | ACTTGAGAAA | GCTGACTTAC | TAAAGGCTAT | TCAAGAACAA | TTGATCGCTA |
| 401 | ACGTCCACAG | TAACGACGAC | TACTTTGAGG | TCATTTGATTT | TGCAACCGAT |
| 451 | GCAACCATT | CTGATCGAAA | CGGCAAGGTC | TACTTTGCTG | ACAAAGATGG |
| 501 | TCGGTAAACC | TTGCCGACCC | AACCTGTCCA | AGAATTTTG | CTAAGCGGAC |
| 551 | ATGTGCGCGT | TAGACCATAT | AAAGAAAAAC | CAATACAAA | CCAAGCGAAA |
| 601 | TCTGTTGATG | TGGAATATAC | TGTACAGTTT | ACTCCCCTAA | ACCCCTGATGA |
| 651 | CGATTTCAGA | CCAGGTCTCA | AAGATACTAA | GCTATTGAAA | ACACTAGCTA |
| 701 | TCGGTGACAC | CATCACATCT | CAAGAATTAC | TAGCTCAAGC | ACAAAGCATT |
| 751 | TTAAACAAAAA | ACCACCCAGG | CTATACGATT | TATGAACGTG | ACTCCTCAAT |
| 801 | CGTCACTCAT | GACAATGACA | TTT TCCGTAC | GATTTTACCA | ATGGATCAAG |
| 851 | AGTTTACTTA | CCGTGTAAA | AATCGGGAAC | AAGCTTATAG | GATCAATAAA |
| 901 | AAATCTGGTC | TGAATGAAGA | AATAAACAC | ACTGACCTGA | TCTCTGAGAA |
| 951 | ATATTACGTC | CTTAAAAAAG | GGGAAAAGCC | GTATGATCCC | TTTGTATCGCA |
| 1001 | GTCACITGAA | ACTGTTCAC | ATCAAATACG | TTGATGTCGA | TACCAACGAA |
| 1051 | TTGCTAAAAA | GTGAGCAGCT | CTTAACAGCT | AGCGAACGTA | ACTTAGACTT |
| 1101 | CAGAGATT | TACGATCCTC | GTGATAAGGC | TAAACTACTC | TACAACAATC |
| 1151 | TCGATGCTT | TGGTATTATG | GACTATACCT | TAACTGGAAA | AGTAGAGGAT |
| 1201 | AATCACGATG | ACACCAACCG | TATCATAACC | GTTTATATGG | GCAAGCGACC |
| 1251 | CGAAGGAGAG | AATGCTAGCT | ATCATTTAGC | CTATGATAAA | GATCGTTATA |
| 1301 | CCGAAGAAGA | ACGAGAAGTT | TACAGCTACC | TGCGTTATAC | AGGGACACCT |
| | ATACCTGATA | ACCCTAACGA | CAAATAA | | |

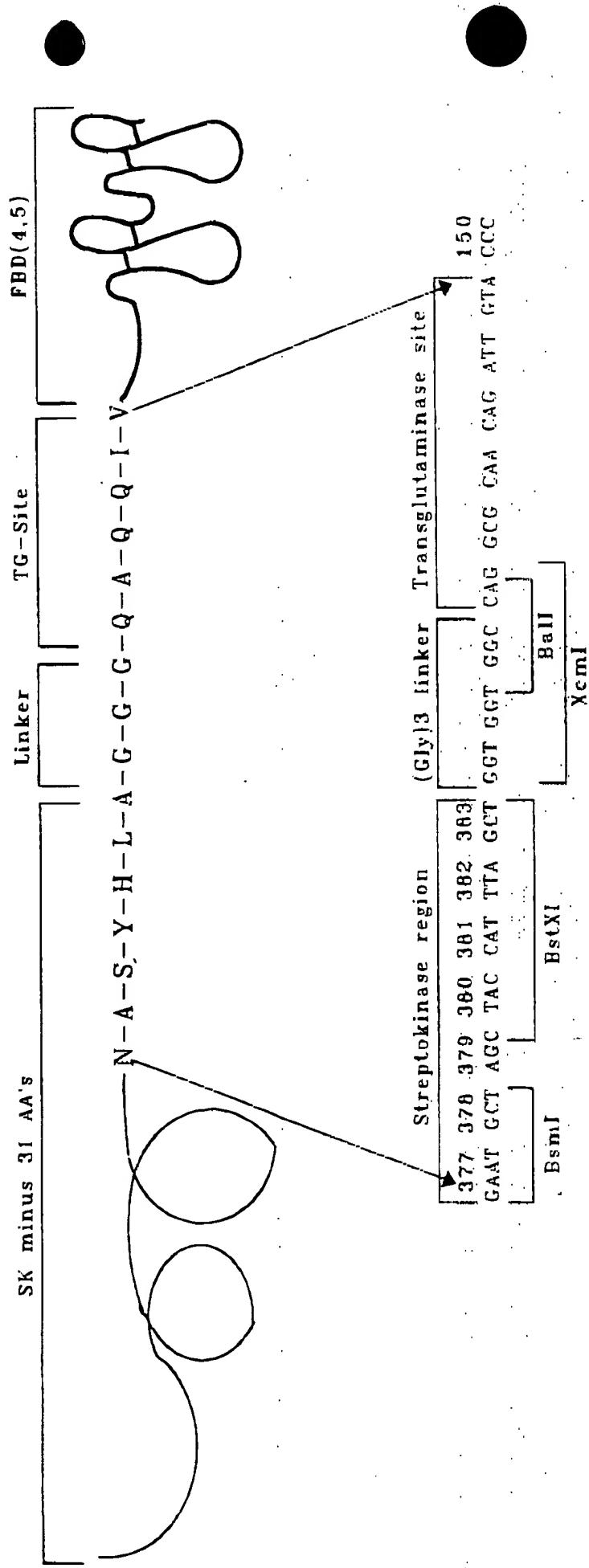
Fig. 15

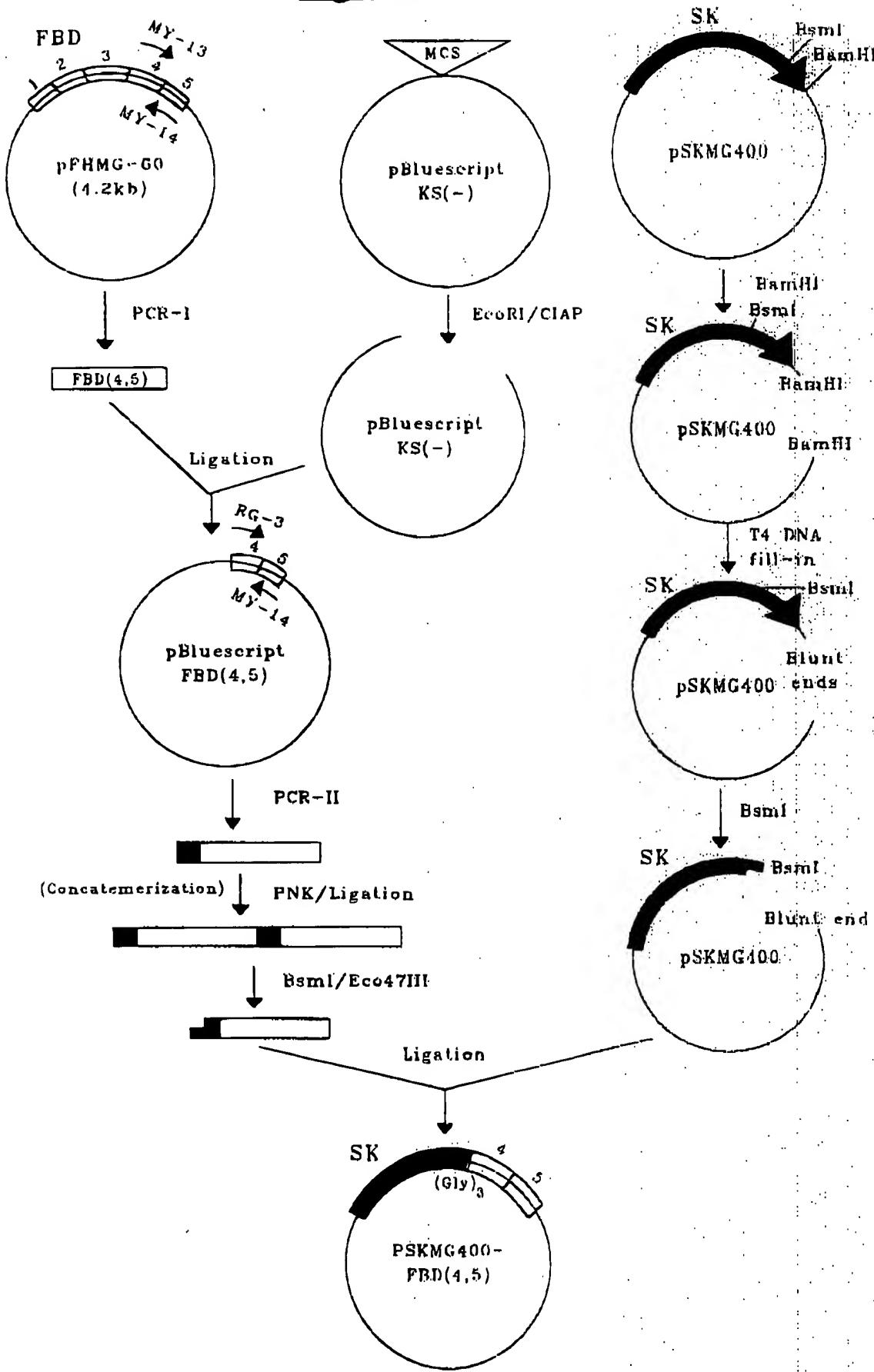
Fig. 16

Fig. 17a

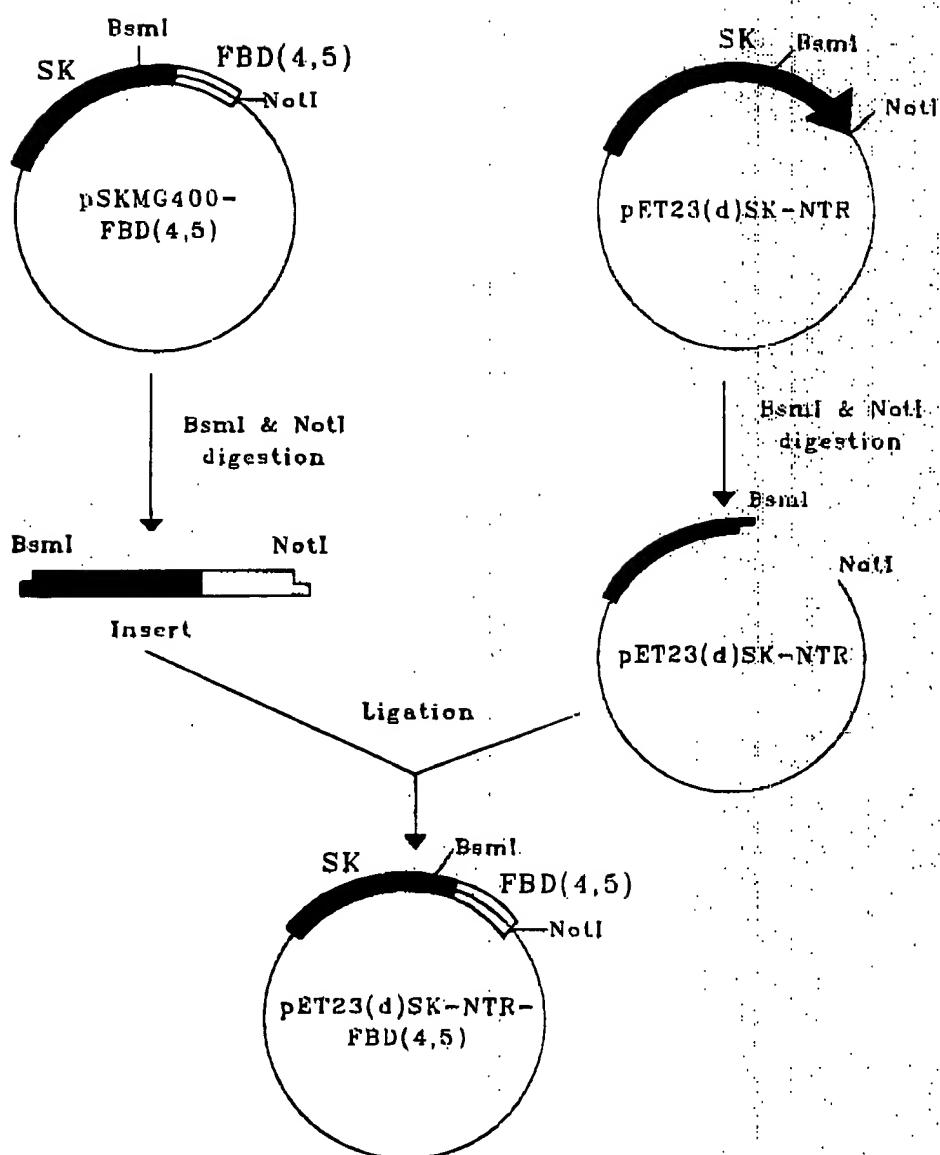


Fig. 17b

| | 10 | 20 | 30 | 40 | 50 |
|------|-------------|------------|-------------|-------------|-------------|
| 51 | TTTGTAAAC | TTAAGAAGG | AGATATACCA | TGATAGCTGG | TCCGTAACTGG |
| 101 | CTACTAGATC | GTCCTTCTGT | AAATAACAGC | CAATTGGTTG | TTAGCGTTGC |
| 151 | TGGTACTGTT | GAGGGGACGA | ATCAAGACAT | TAGTCTTAAG | TTTTTTGAAA |
| 201 | TCGATCTAAC | ATCACGACCT | GCTCATGGAG | GAAAGACAGA | GCAAGGCCTA |
| 251 | AGTCCAAAAT | CAAACCATT | TGCTACTGAT | AGTGGCGCGA | TGTACATCAA |
| 301 | ACTTGAGAAA | GCTGACTTAC | TA AAGGCTAT | TCAAGAACAA | TTGATCGCTA |
| 351 | ACGTCCACAG | TAACGACGAC | TACTTTGAGG | TCATTGATIT | TGCAAGCGAT |
| 401 | GCAACCATT | CTGATCGAAA | CGGCAAGGTC | TACTTTGCTG | ACAAAGATGG |
| 451 | TTCGGTAACC | TTGCCGACCC | AACCTGTCCA | AGAATTTTG | CTAAGCGGAC |
| 501 | ATGTGCGCGT | TAGACCATAT | AAAGAAAAAC | CAATACAAAA | CCAAGCGAAA |
| 551 | TCTGTTGATG | TGGAATATAC | TGTACAGTTT | ACTCCCTTAA | ACCCGTATGA |
| 601 | CGATTTCAGA | CCAGGTCTCA | AAGATACTAA | GCTATTGAAA | ACACTAGCTA |
| 651 | TCGGTGACAC | CATCACATCT | CAAGAATTAC | TAGCTCAAGC | ACAAAGCATT |
| 701 | TTAAACAAAA | ACCACCCAGG | CTATACGATT | TATGAACGTG | ACTCCTCAAT |
| 751 | CGTCACTCAT | GACAATGACA | TTTCCGTAC | GATTTACCA | ATGGATCAAG |
| 801 | AGTTTACTTA | CCGTGTTAAA | AATCGGGAAC | AAGCTTATAG | GATCAATAAA |
| 851 | AAATCTGGTC | TGAATGAAGA | AATAAAACAC | ACTGACCTGA | TCTCTGAGAA |
| 901 | ATATTACGTC | CTTAAAAAAG | GGGAAAAGCC | GTATGATCCC | TTGATCGCA |
| 951 | GTCACTTGAA | ACTGTTCACC | ATCAAATACG | TTGATGTCGA | TACCAACGAA |
| 1001 | TTGCTAAAAAA | GTGAGCAGCT | CTTAAACAGCT | AGCGAACGTA | ACTTAGACTT |
| 1051 | CAGAGATTTA | TACGATCCTC | GTGATAAGGC | TAAACTACTC | TACAACAATC |
| 1101 | TCGATGCTTT | TGGTATTATG | GAECTATACCT | TAACCTGGAAA | AGTAGAGGAT |
| 1151 | AATCACGATG | ACACCAACCG | TATCATAACC | GTTTATATGG | GCAAGCGACC |
| 1201 | CGAAGGAGAG | AATGCTAGCT | ACCATTAGC | TGGTGGTGGC | CAGGCACAAAC |
| 1251 | AGATTGTACC | CATAGCTGAG | AAGTGTGGT | ATCATGCTGC | TGGGACTTCC |
| 1301 | TATGTGGTCG | GAGAAACGTG | GGAGAAAGCCC | TACCAAGGCT | GGATGATGGT |
| 1351 | AGATTGTACT | TGCCTGGGAG | AAGGCAGCGG | ACGCATCACT | TGCACTTCTA |
| 1401 | GAAATAGATG | CAACGATCAG | GACACAAGGA | CATCCTATAG | AATTGGAGAC |
| 1451 | ACCTGGAGCA | AGAAGGATAA | TCGAGGAAAC | CTGCTCCAGT | GCATCTGCAC |
| 1501 | AGGCAACGGC | CGAGGAGAGT | GGAAGTGTGA | GAGGCACACC | TCTGTGCAGA |
| | CCACATCGAG | CGGATCTGGC | CCCTTCACCG | ATGTTCGTTA | G |

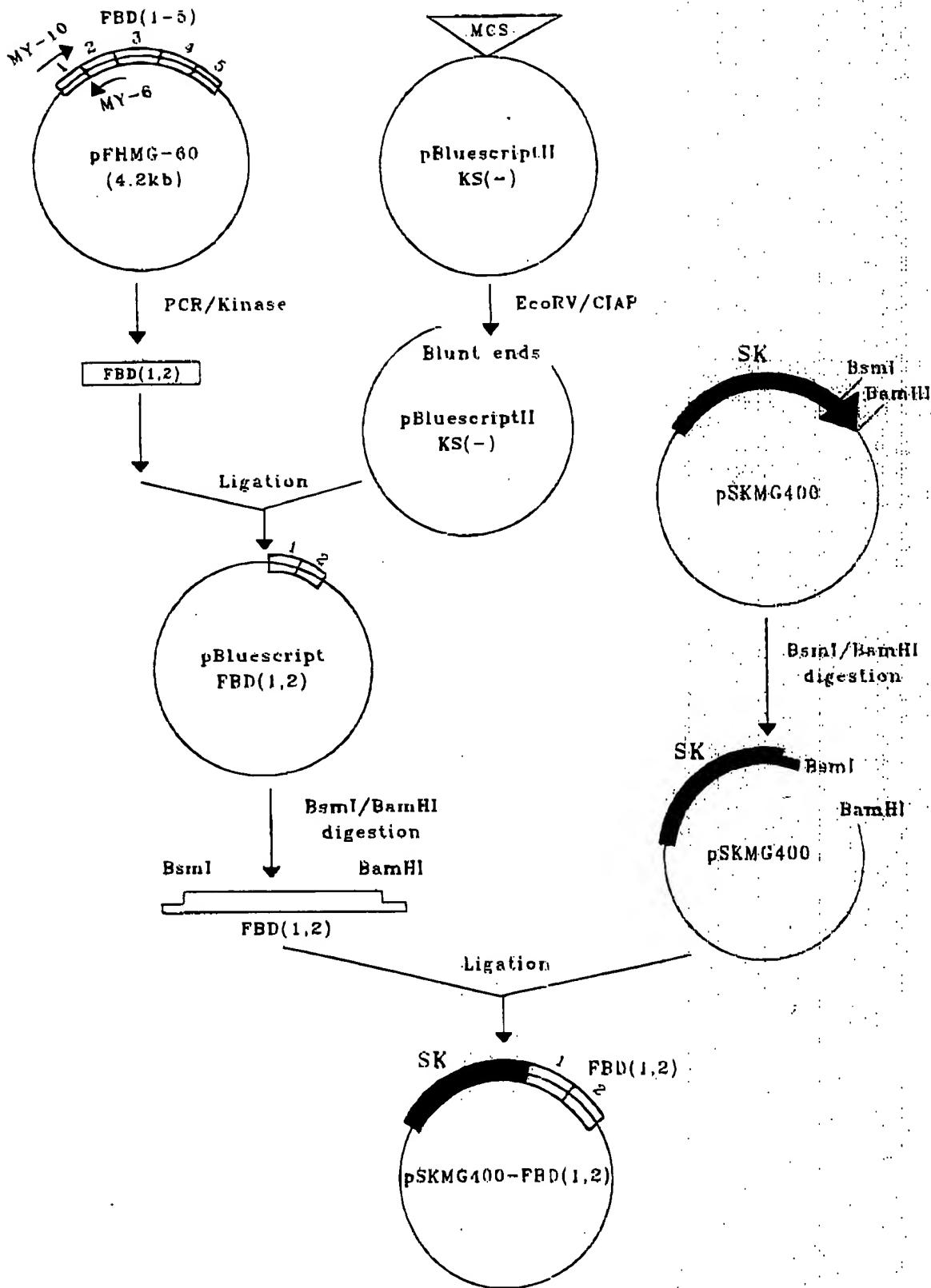
Fig. 18

Fig. 19a

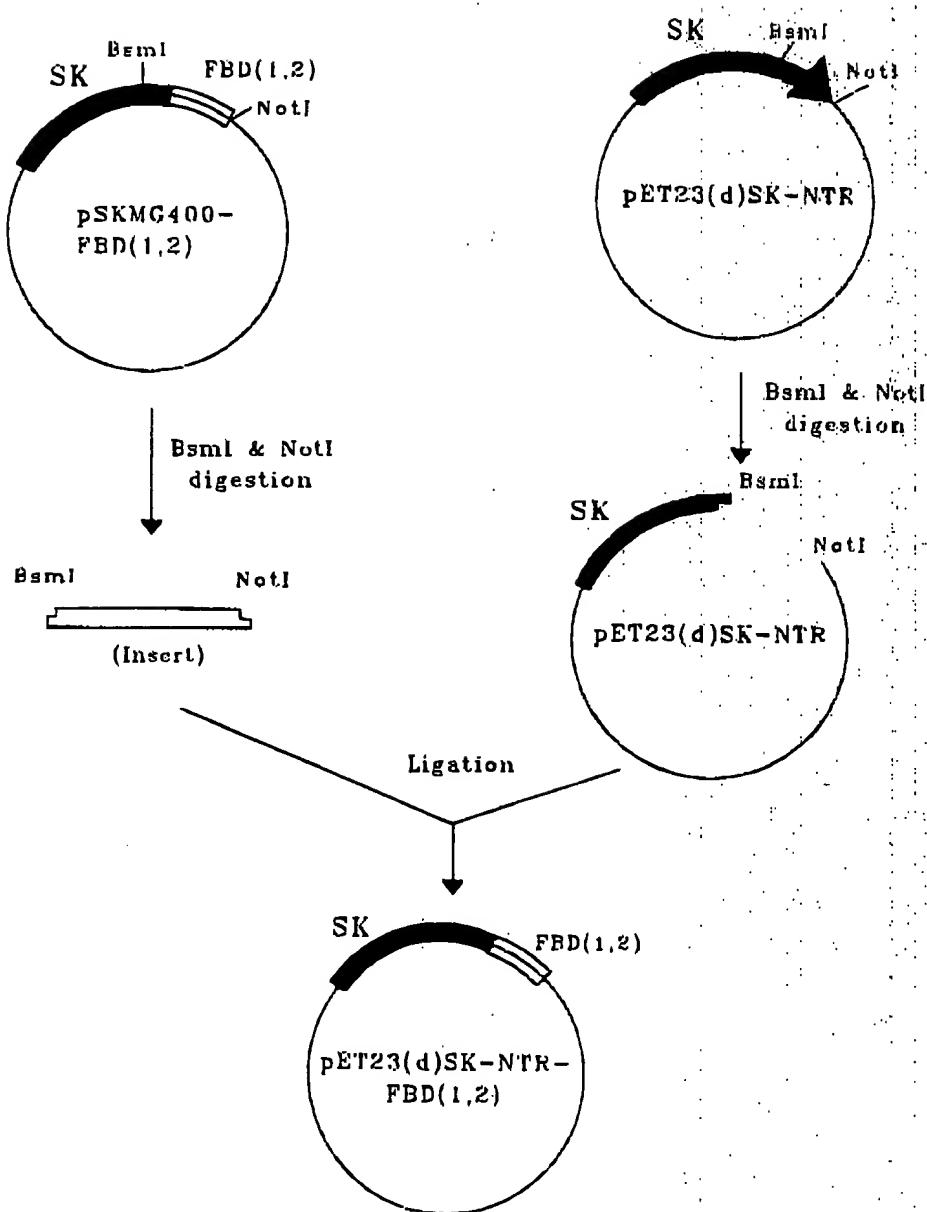


Fig. 19b

| 10 | 20 | 30 | 40 | 50 |
|------------------|-------------|-------------|-------------|--------------|
| 51 GCAACCCCGC | CAGCCTAGCC | GGGTCTCAA | CGACAGGAGC | ACGATCATGC |
| 101 GCACCCGTGG | CCAGGACCCA | ACGCTGCCG | AGATCTCGAT | CCC CGA AAAT |
| 151 TAATACGACT | CACTATAGGG | AGACCACAAC | GGTTTCCCTC | TAGAAATAAT |
| 201 CTGCTAGACC | GTCCATCTGT | CAACAACAGC | TGATTGCTGG | ACCTGAGTGG |
| 251 TGGTACTGTT | GAGGGGACGA | ATCAAGACAT | CAATTGGTGTG | TTAGCGTTC |
| 301 TCGATCTAAC | ATCACCGACCT | GCTCATGGAG | TAGTCTTAAA | TTTTTGAAA |
| 351 AGTCCAAAAT | CAAAACCATT | TGCTACTGTAT | GAAAGACAGA | GCAAGGCTTA |
| 401 ACTTGAGAAA | GCTGACITAC | TAAAGGCTAT | AGTGGCGCGA | TGTCACATAA |
| 451 ACGTCCACAG | TAACGACGAC | TACTTTGAGG | TCAAGAACAA | TTGATCGCTA |
| 501 GCAACCATT | CTGATCGAAA | CGGCAAGGTC | TCATTGATT | TGCAAGCGAT |
| 551 TTCGGTAACC | TTGCCGACCC | AACCTGTCCA | TACTTTGCTG | ACAAAGATGG |
| 601 ATGTGCGCGT | TAGACCATAT | AAAGAAAAAC | AGAATTTTG | CTAAGCGGAC |
| 651 TCTGTTGATG | TGGAATATAC | TGTACAGTTT | CAATACAAA | CCAAGCGAAA |
| 701 CGATTTAGA | CCAGGTCTCA | AAGATACTAA | ACTCCCTTAA | ACCCCTGATGA |
| 751 TCGGTGACAC | CATCACATCT | CAAGAATTAC | GCTATTGAAA | ACACTAGCTA |
| 801 TTAAACAAAAA | ACCACCCAGG | CTATACGATT | TAGCTCAAGC | ACAAAGCATT |
| 851 CGTCACTCAT | GACAATGACA | TTTCCGTAC | TATGAACGTG | ACTCCTCAAT |
| 901 AGTTTACTTA | CCGTGTTAAA | AATCGGGAAC | GATTTACCA | ATGGATCAAG |
| 951 AAATCTGGTC | TGAATGAAGA | AATAAACAAAC | AAGCTTATAG | GATCAATAAA |
| 1001 ATATTACGTC | CTTAAAAAAG | GGGAAAAGCC | ACTGACCTGA | TCTCTGAGAA |
| 1051 GTCACTTGAA | ACTGTTCAC | ATCAAATACG | GTATGATCCC | TTTGATCGCA |
| 1101 TTGCTAAAAAA | GTGAGCAGCT | CTTAACAGCT | TTGATGTCGA | TACCAACCGAA |
| 1151 CAGAGATTTA | TACGATCCTC | GTGATAAGGC | AGCGAACGIA | ACTTAGACIT |
| 1201 TCGATGCTTT | TGGTATTATG | GACTATACCT | TAAACTACTC | TACAACAAATC |
| 1251 AATCACGATG | ACACCAACCG | TATCATAACC | TAAC TGAAA | AGTAGAGGGAT |
| 1301 CGAAGGAGAG | AATGCTAGCT | ATCATTAGC | GTTTATATGG | GCAAGCGGAC |
| 1351 AAATGGTTCA | GCCCCAGTCC | CCGGTGGCTG | CGGTGGTGGT | CAGGCAGCAGC |
| 1401 TGTTATGACA | ATGGAAAACA | CTATCAAGATA | TCAGTCAAAG | CAAGCCCCGT |
| 1451 CTACCTAGGT | AATGTGTGG | TTTGTACTTG | AATCAACAGT | GGGAGCGGAC |
| 1501 TTAACTGCGA | AAGTAAACCT | GAAGCTGAAG | TTATGGAGGA | AGCCGAGGTT |
| 1551 ACTGGGAACA | CTTACCGAGT | GGGTGACACT | AGACTTGCTT | TGACAAGTAC |
| 1601 CATGATCTGG | GAATGTACCT | GCATCGGGGC | TATGAGCGTC | CTAAAGACTC |
| 1651 GTACCATCTA | A | | | AGAATAAGCT |

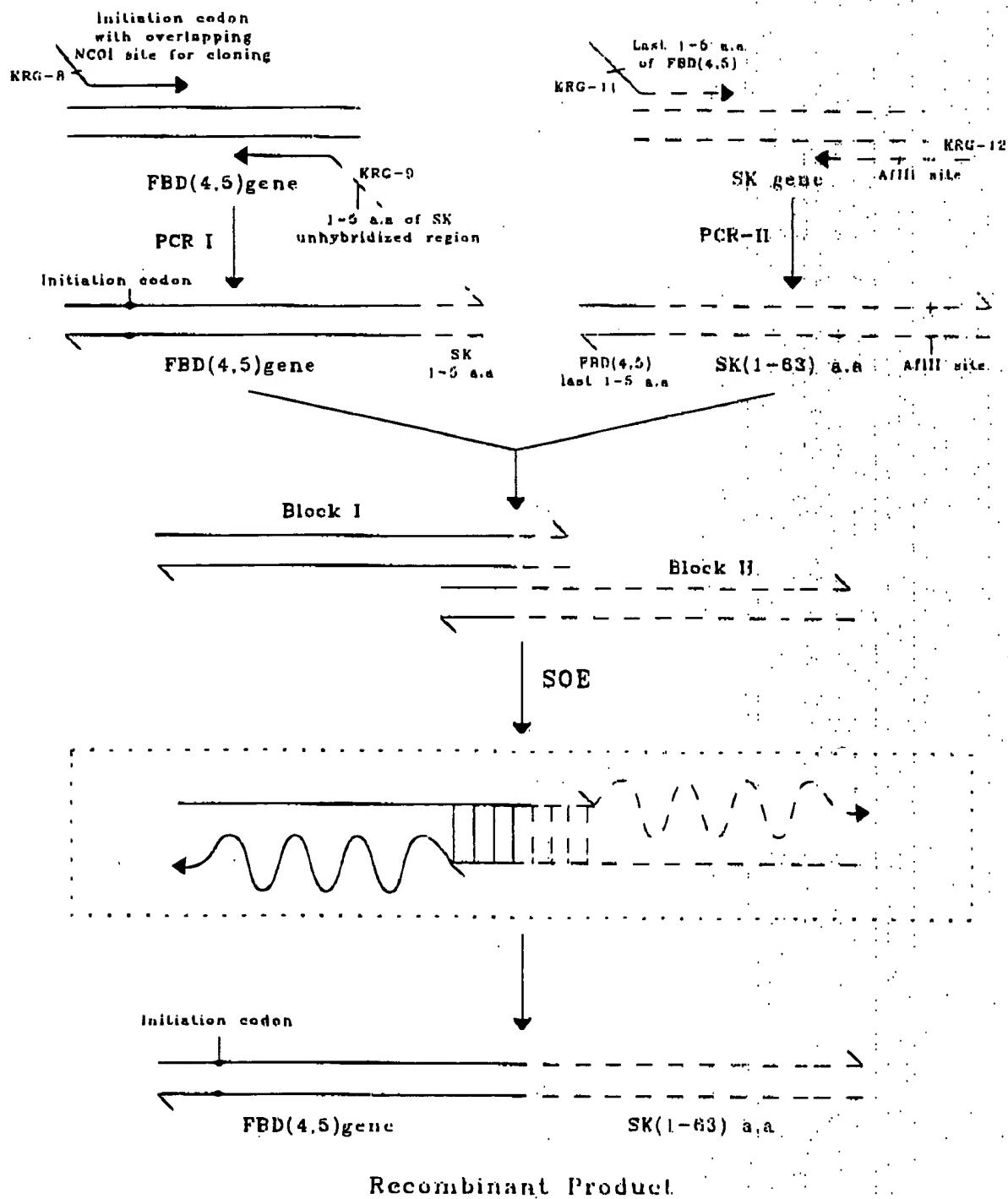
Fig. 20

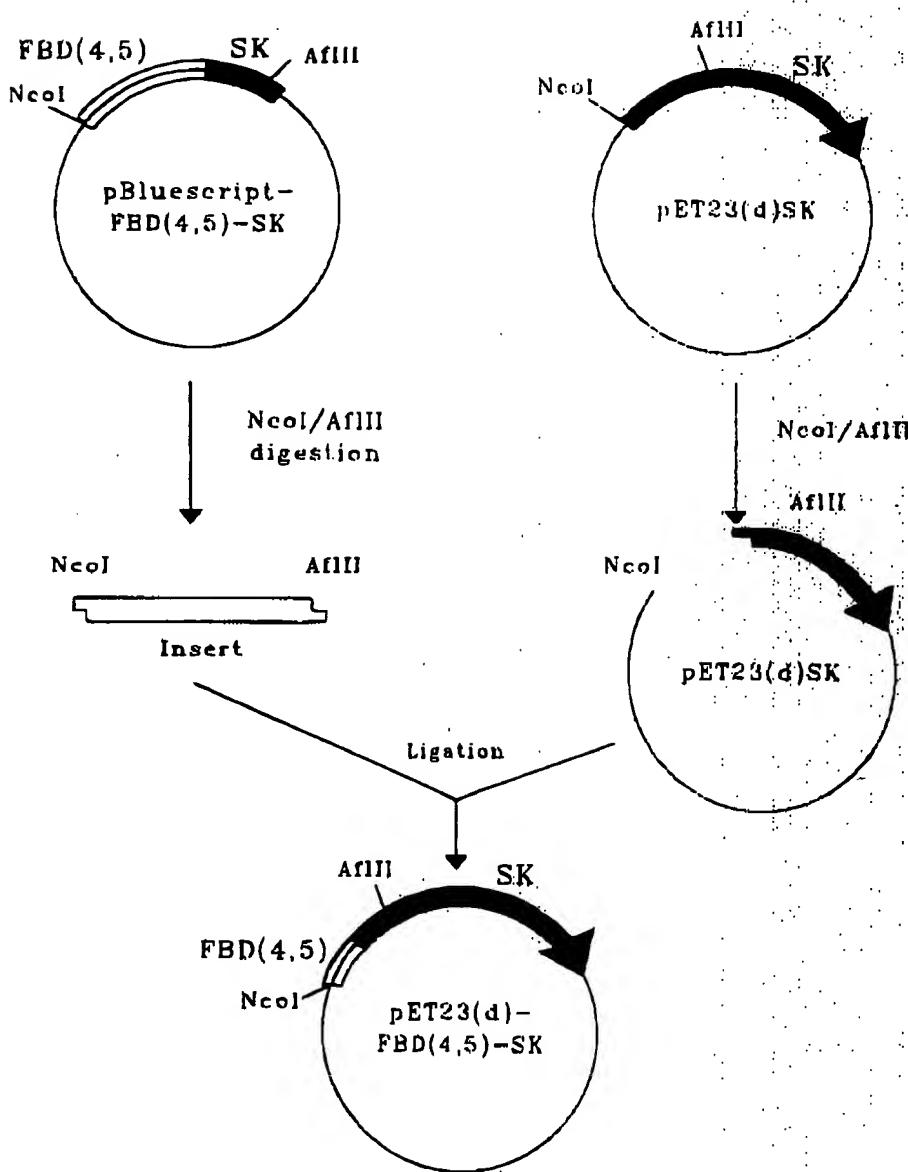
Fig. 21a

Fig. 21b

| | 10 | 20 | 30 | 40 | 50 |
|------|------------|-------------|------------|-------------|-------------|
| 1 | TCGCTTCACG | TTCGCTCGCG | TATCGGTGAT | TCATTCTGCT | AACCAGTAAG |
| 51 | GCAACCCCGC | CAGCCTAGCC | GGGTCTCAA | CGACAGGAGC | ACGATCATGC |
| 101 | GCACCCGTGG | CCAGGACCCA | ACGCTGCCCG | AGATCTCGAT | CCCGCGAAAT |
| 151 | TAATACGACT | CACTATAGGG | AGACCACAAC | GGTTTCCCTC | TAGAAATAAT |
| 201 | TTTGTAAAC | TTAAAGAAGG | AGATATACCA | TGGTGAAGC | ACAACAGATT |
| 251 | GTACCCATAG | CTGAGAAGTG | TTTGATCAT | GCTGCTGGGA | CTTCCTATGT |
| 301 | GGTCGGAGAA | ACGTGGGAGA | AGGCAGCGGA | CGCATCACTT | GCACCTCTAG |
| 351 | AAATAGATGC | AACGATCAGG | ACACAAGGAC | ATCCTATAGA | ATTGGAGACA |
| 401 | CCTGGAGCAA | GAAGGATAAT | CGAGGAAACC | TGCTCCAGTG | CATCTGCACA |
| 451 | GGCAACGGCC | GAGGAGAGTG | GAAGTGTGAG | AGGCACACCI | CTGTGCAGAC |
| 501 | CACATCGAGC | GGATCTGGCC | CCTTCACCGA | TGTTCGTATT | GCTGGACCTG |
| 551 | AGTGGCTGCT | AGACCGTCCA | TCTGTCAACA | ACAGCCAATT | GGTTGTTAGC |
| 601 | GTTGCTGGTA | CTGTTGAGGG | GACGAATCAA | GACATTAGTC | TTAAATTTTT |
| 651 | TGAAATCGAT | CTAACATCAC | GACCTGCTCA | TGGAGGAAAG | ACAGAGCAAG |
| 701 | GCTTAAGTCC | AAAATCAAAA | CCATTGCTA | CTGATAGTGG | CGCGATGTCA |
| 751 | CATAAACTTG | AGAAAGCTGA | CTTACTAAAG | GCTATTCAAG | AACAATTGAT |
| 801 | CGCTAACGTC | CACAGTAACC | ACGACTACTT | TGAGGTCACTT | GATTTTGCAA |
| 851 | GCGATGCAAC | CATTACTGAT | CGAAACGGCA | AGGTCTACTT | TGCTGACAAA |
| 901 | GATGGTTCGG | TAACCTGCC | GACCCAACCT | GTCCAAGAAT | TTTGCTAAG |
| 951 | CGGACATGTG | CGCGTTAGAC | CATATAAAGA | AAAACCAATA | CAAAACCAAG |
| 1001 | CGAAATCTGT | TGATGTGGAA | TATACTGTAC | AGTTTACTCC | CTTAAACCCCT |
| 1051 | GATGACGATT | TCAGACCAGG | TCTCAAAGAT | ACTAAGCTAT | TGAAAACACT |
| 1101 | AGCTATCGGT | GACACCATCA | CATCTCAAGA | ATTACTAGCT | CAAGCACAAA |
| 1151 | GCATTTAAA | CAAAAACAC | CCAGGCTATA | CGATTATGA | ACGTGACTCC |
| 1201 | TCAATCGTCA | CTCATGACAA | TGACATTTC | CGTACGATT | TACCAATGGA |
| 1251 | TCAAGAGTTT | ACTTACCGTG | TTAAAAATCG | GGAACAAGCT | TATAGGATCA |
| 1301 | ATAAAAAATC | TGGTCTGAAT | GAAGAAATAA | ACAACACTGA | CCTGATCTCT |
| 1351 | GAGAAATATT | ACGTCTTAA | AAAAGGGAA | AAGCCGTATG | ATCCCCTTGA |
| 1401 | TCGCAGTCAC | TTGAAACTGT | TCACCCTCAA | ATACGTTGAT | GTCGATACCA |
| 1451 | ACGAATTGCT | AAAAAGTGAG | CAGCTCTAA | CAGCTAGCGA | ACGTAACCTA |
| 1501 | GAATTCAAG | ATTTATACGA | TCCTCGTGT | AAGGCTAAAC | TACTCTACAA |
| 1551 | CAATCTGAT | GCTTTGGTA | TTATGGACTA | TACCTTAACT | GGAAAAGTAG |
| 1601 | AGGATAATCA | CGATGACACC | AACCGTATCA | TAACCGTTA | TATGGGCAAG |
| 1651 | CGACCCGAAG | GAGAGAATGC | TAGCTATCAT | TTAGCCTATG | ATAAAGATCG |
| 1701 | TTATACCGAA | GAAGAACGAG | AAGTTTACAG | CTACCTCGT | TATACAGGGAA |
| 1751 | CACCTATACC | TGATAACCCCT | AACGACAAAT | AA | |

Fig. 22a

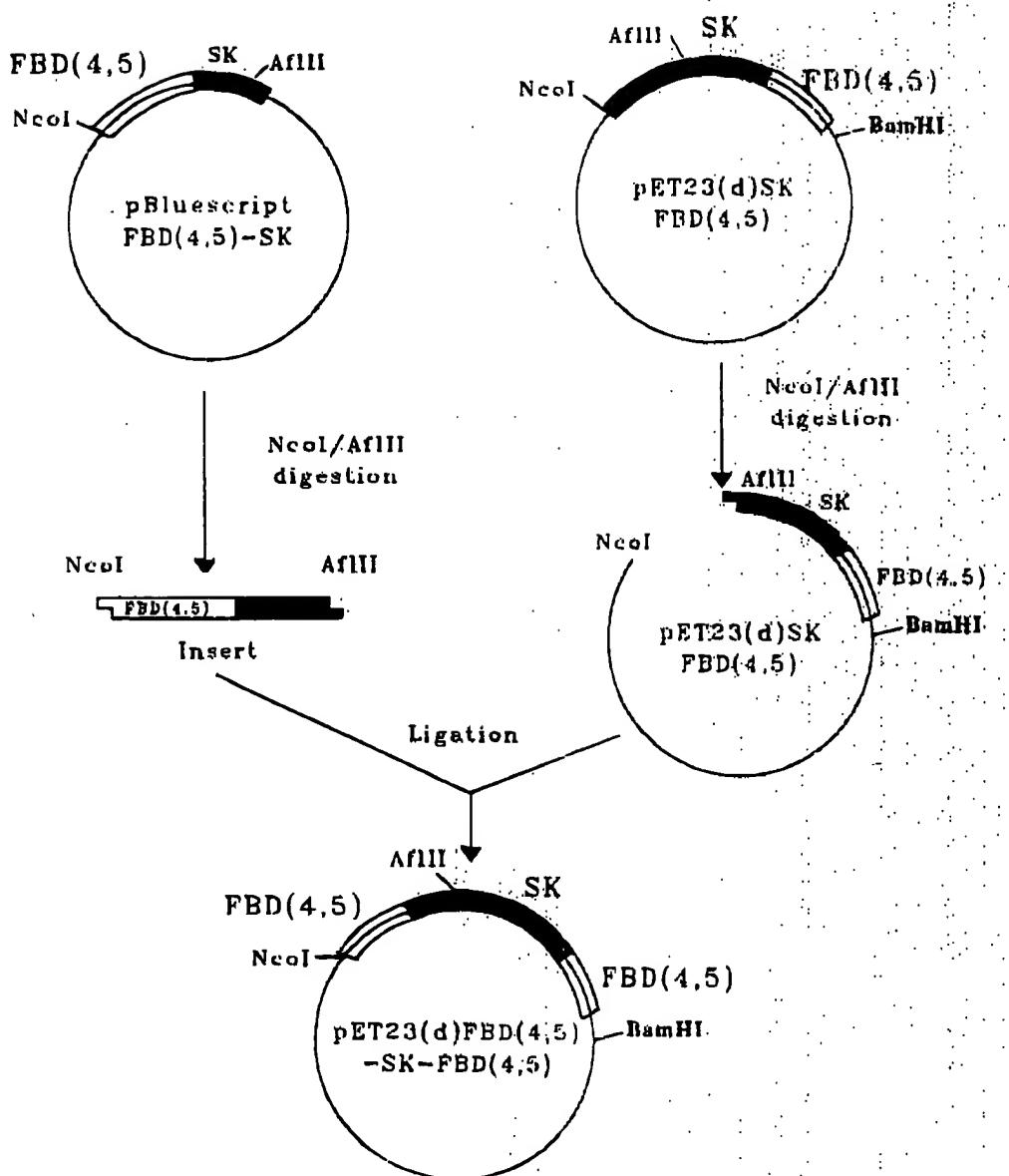


Fig. 22b

| | 10 | 20 | 30 | 40 | 50 |
|------|-------------|-------------|-------------|-------------|------------|
| 1 | CGAAGACCAT | TCATGTTGTT | GCTCAGGTGCG | CAGACGTTT | GCAGCAGCAG |
| 51 | TCGCTTCACG | TTCGCTCGCG | TATCGGTGAT | TCATTCTGCT | AACCAGTAAG |
| 101 | GCAACCCCGC | CAGCCTAGCC | GGGTCCCAA | CGACAGGAGC | ACGATCATGC |
| 151 | GCACCCGTGG | CCAGGACCCA | ACGCTGCCG | AGATCTCGAT | CCCGCGAAAT |
| 201 | TAATACGACT | CACTATAGGG | AGACCACAAC | GGTTTCECTC | TAGAAATAAT |
| 251 | TTTGTAAAC | TTAAGAAGG | AGATATACCA | TGGTGCAAGC | ACAACAGATT |
| 301 | GTACCCATAG | CTGAGAAGTG | TTTTGATCAT | GCTGCTGGGA | CTTCCTATGT |
| 351 | GGTCGGAGAA | ACGTGGGAGA | AGGCAGCGGA | CGCATCACTT | GCACTTCTAG |
| 401 | AAATAGATGC | AACGATCAGG | ACACAAGGAC | ATCCTATAGA | ATTGGAGACA |
| 451 | CCTGGAGCAA | GAAGGATAAT | CGAGGAAACC | TGCTCCAGTG | CATCTGCACA |
| 501 | GGCAACGGCC | GAGGAGAGTG | GAAGTGTGAG | AGGCACACCT | CTGTGCAGAC |
| 551 | CACATCGAGC | GGATCTGGCC | CTTTCACCGA | TGTTCGTATT | GCTGGACCTG |
| 601 | AGTGGCTGCT | AGACCGTCCA | TCTGTCAACA | ACAGCCAATT | GGTTGTTAGC |
| 651 | GTTGCTGGTA | CTGTTGAGGG | GACGAATCAA | GACATTAGTC | TTAAATTTTT |
| 701 | TGAAATCGAT | CTAACATCAC | GACCTGCTCA | TGGAGGAAAG | ACAGAGCAAG |
| 751 | GCTTAAGTCC | AAAATCAAAA | CCATTGCTA | CTGATAGTGG | CGCGATGTCA |
| 801 | CATAAACTTG | AGAAAAGCTGA | CITACTAAAG | GCTATTCAAG | AACAATTGAT |
| 851 | CGCTAACGTC | CACAGTAACG | ACGACTACTT | TGAGGTCATT | GATTTTGCAA |
| 901 | GCGATGCAAC | CATTACTGAT | CGAAACGGCA | AGGTCTACTT | TGCTGACAAA |
| 951 | GATGGTTCGG | TAACCTTGCC | GACCCAACTT | GTCCAAGAAT | TTTGCTAAG |
| 1001 | CGGACATGTG | CGCGTTAGAC | CATATAAAGA | AAAACCAATA | CAAAACCAAG |
| 1051 | CGAAATCTGT | TGATGTGAA | TATACTGTAC | AGTTTACTCC | CITAAACCT |
| 1101 | GATGACGATT | TCAGACCAGG | TCTCAAAGAT | ACTAAGCTAT | TGAAAACACT |
| 1151 | AGCTATCGGT | GACACCATCA | CATCTCAAGA | ATTACTAGCT | CAAGCACAAA |
| 1201 | GCATTTAAA | CAAAAACCAC | CCAGGTATA | CGATTATGA | ACGTGAATCC |
| 1251 | TCAATCGTC | CTCATGACAA | TGACATTTC | CGTACGATIT | TACCAATGG |
| 1301 | TCAAGAGTTT | ACTTACCGTG | TTAAAAATCG | GGAAACAAGCT | TATAGGATCA |
| 1351 | ATAAAAAAATC | TGGTCTGAAT | GAAGAAATAA | ACAACACTGA | CCTGATCTCT |
| 1401 | GAGAAATATT | ACGTCTTAA | AAAAGGGAA | AAGCCGTATG | ATCCCTTGA |
| 1451 | TCGCAGTCAC | TTGAAACTGT | TCACCATCAA | ATACGTTGAT | GTCGATACCA |
| 1501 | ACGAATTGCT | AAAAAGTGAG | CAGCTCTTAA | CAGCTAGCGA | ACGTAACCTA |
| 1551 | GACTTCAGAG | ATTTATACGA | TCCTCGTGT | AAGGCTAAC | TACTCTACAA |
| 1601 | CAATCTCGAT | GCTTTGGTA | TTATGGACTA | TACCTTAAC | GGAAAAGTAG |
| 1651 | AGGATAATCA | CGATGACACC | AACCGTATCA | TAACCGTTA | TATGGGCAAG |
| 1701 | CGACCCGAAG | GAGAGAATGC | TAGCTACCAT | TTAGCTGGTG | GTGGCCAGGC |
| 1751 | GCAACAGATT | GTACCCATAG | CTGAGAAGTG | TTTGATCAT | GCTGCTGG |
| 1801 | CTTCCTATGT | GGTCGGAGAA | ACGTGGGACIA | AGCCCTACCA | AGGCTGGATG |
| 1851 | ATGGTAGATT | GTACTTGCCT | GGGAGAAGGC | AGCGGACGCA | TCACTTGCAC |
| 1901 | TTCTAGAAAT | AGATGCAACG | ATCAGGACAC | AAGGACATCC | TATAGAATTG |
| 1951 | GAGACACCTG | GAGCAAGAAG | GATAATCGAG | GAAACCTGCT | CCAGTGCATC |
| 2001 | TGCACAGGCA | ACGGCCGAGG | AGAGTGGAAAG | TGTGAGAGGC | ACACCTCTGT |
| 2051 | GCAGACCA | TCGAGCGGAT | CTGGCCCCCTT | CACCGATGTT | CGTTAG |

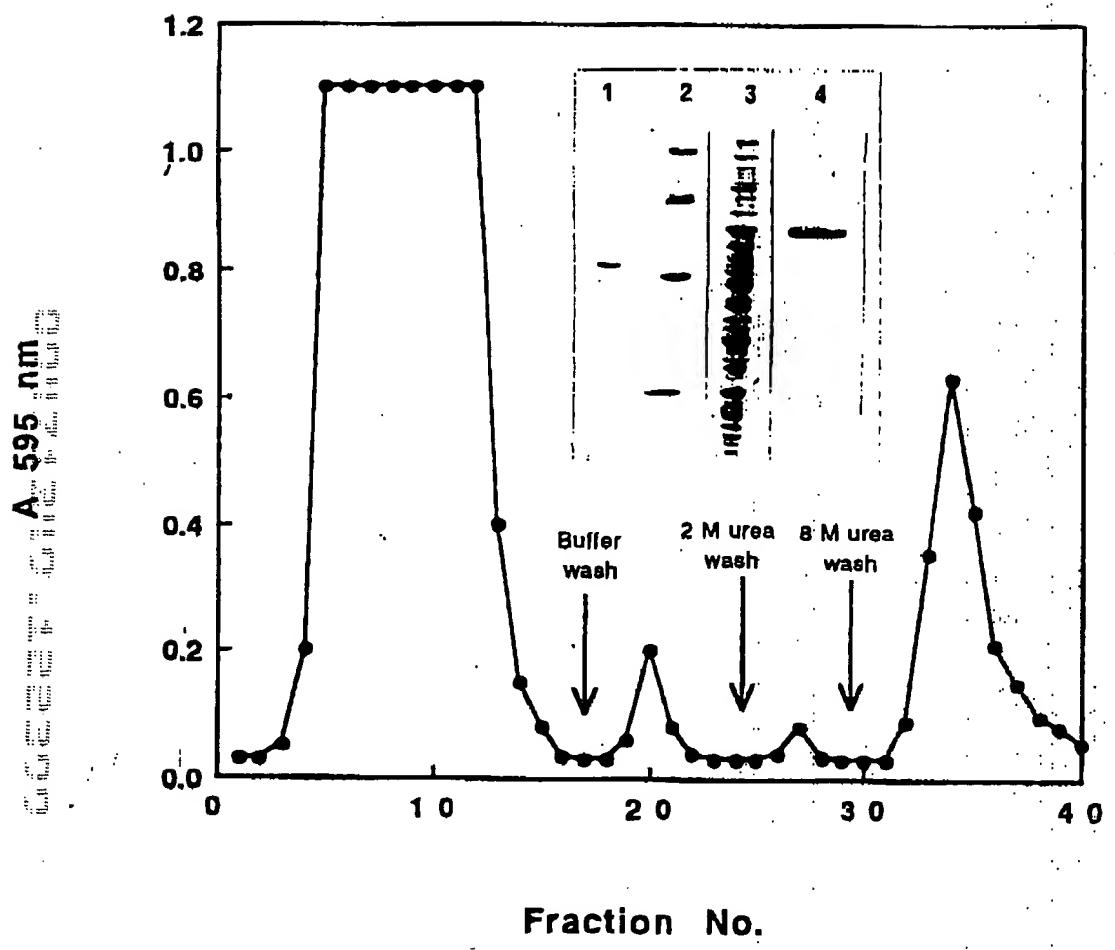
Fig. 23

Fig. 24

